



#3

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SEQUENCE LISTING

<110> Chen, Ruoping
Chu, Zhi Liang
Dang, Huong T.
Lowitz, Kevin P.
Pride, Cameron

<120> Endogenous And Non-Endogenous Versions of Human G Protein-Coupled Receptors

<130> AREN-0308

<140> 09/995,225
<141> 2001-11-26

<150> 09/170,496
<151> 1998-10-13

<150> PCT/US99/23938
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<150> 60/253,404
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 gtccacgtgg cactgcagat ccccttcaat gtgtcctcac tgggtggccat gtactccacc 360
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Pro Ala Cys Gln Asp Leu Gln Leu Gly Leu Ser Leu Leu Ser Leu Leu
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Gly Leu Val Val Gly Val Pro Val Gly Leu Cys Tyr Asn Ala Leu Leu
 35 40 45

Val Leu Ala Asn Leu His Ser Lys Ala Ser Met Thr Met Pro Asp Val
 50 55 60

Tyr Phe Val Asn Met Ala Val Ala Gly Leu Val Leu Ser Ala Leu Ala
 65 70 75 80

Pro Val His Leu Leu Gly Pro Pro Ser Ser Arg Trp Ala Leu Trp Ser

85

90

95

Val Gly Gly Glu Val His Val Ala Leu Gln Ile Pro Phe Asn Val Ser
 100 105 110

Ser Leu Val Ala Met Tyr Ser Thr Ala Leu Leu Ser Leu Asp His Tyr
 115 120 125

Ile Glu Arg Ala Leu Pro Arg Thr Tyr Met Ala Ser Val Tyr Asn Thr
 130 135 140

Arg His Val Cys Gly Phe Val Trp Gly Gly Ala Leu Leu Thr Ser Phe
 145 150 155 160

Ser Ser Leu Leu Phe Tyr Ile Cys Ser His Val Ser Thr Arg Ala Leu
 165 170 175

Glu Cys Ala Lys Met Gln Asn Ala Glu Ala Ala Asp Ala Thr Leu Val
 180 185 190

Phe Ile Gly Tyr Val Val Pro Ala Leu Ala Thr Leu Tyr Ala Leu Val
 195 200 205

Leu Leu Ser Arg Val Arg Arg Glu Asp Thr Pro Leu Asp Arg Asp Thr
 210 215 220

Gly Arg Leu Glu Pro Ser Ala His Arg Leu Leu Val Ala Thr Val Cys
 225 230 235 240

Thr Gln Phe Gly Leu Trp Thr Pro His Tyr Leu Ile Leu Leu Gly His
 245 250 255

Thr Val Ile Ile Ser Arg Gly Lys Pro Val Asp Ala His Tyr Leu Gly
 260 265 270

Leu Leu His Phe Val Lys Asp Phe Ser Lys Leu Leu Ala Phe Ser Ser
 275 280 285

Ser Phe Val Thr Pro Leu Leu Tyr Arg Tyr Met Asn Gln Ser Phe Pro
 290 295 300

Ser Lys Leu Gln Arg Leu Met Lys Lys Leu Pro Cys Gly Asp Arg His
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Cys Ser Pro Asp His Met Gly Val Gln Gln Val Leu Ala
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<213> Homo sapiens

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<211> 305

<212> PRT

<213> Homo sapiens

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Thr Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu
20              25              30

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Val Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg
35              40              45

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Ser Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val
50              55              60

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Phe Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr
65              70              75              80

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Trp Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His

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85

90

95

Ile His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val Ile Leu Val Thr
 100 105 110

Arg Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val Glu Phe Tyr Arg
 115 120 125

Lys Leu His Ala Val Ala Ala Ser Ala Gly Met Trp Thr Leu Val Ile
 130 135 140

Val Ile Val Val Pro Leu Val Val Ser Arg Tyr Gly Ile His Glu Glu
 145 150 155 160

Tyr Asn Glu Glu His Cys Phe Lys Phe His Lys Glu Leu Ala Tyr Thr
 165 170 175

Tyr Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe Val Ile Ala Val
 180 185 190

Ala Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile Met Leu Met Val
 195 200 205

Gln Lys Leu Arg His Ser Leu Leu Ser His Gln Glu Phe Trp Ala Gln
 210 215 220

Leu Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val Cys Phe Leu Pro
 225 230 235 240

Tyr Gln Phe Phe Arg Ile Tyr Tyr Leu Asn Val Val Thr His Ser Asn
 245 250 255

Ala Cys Asn Ser Lys Val Ala Phe Tyr Asn Glu Ile Phe Leu Ser Val
 260 265 270

Thr Ala Ile Ser Cys Tyr Asp Leu Leu Leu Phe Val Phe Gly Gly Ser
 275 280 285

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Arg
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          20          25          30

Gly Gln Pro Arg Val Thr Leu Leu Pro Thr Pro Asn Val Ser Gly Leu
          35          40          45

Ser Gln Glu Phe Glu Ser His Trp Pro Glu Ile Ala Glu Arg Ser Pro

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50

55

Cys Val Ala Gly Val Ile Pro Val Ile Tyr Tyr Ser Val Leu Leu Gly
65 70 75 80

Leu Gly Leu Pro Val Ser Leu Leu Thr Ala Val Ala Leu Ala Arg Leu
85 90 95

Ala Thr Arg Thr Arg Arg Pro Ser Tyr Tyr Tyr Leu Leu Ala Leu Thr
100 105 110

Ala Ser Asp Ile Ile Ile Gln Val Val Ile Val Phe Ala Gly Phe Leu
115 120 125

Leu Gln Gly Ala Val Leu Ala Arg Gln Val Pro Gln Ala Val Val Arg
130 135 140

Thr Ala Asn Ile Leu Glu Phe Ala Ala Asn His Ala Ser Val Trp Ile
145 150 155 160

Ala Ile Leu Leu Thr Val Asp Arg Tyr Thr Ala Leu Cys His Pro Leu
165 170 175

His His Arg Ala Ala Ser Ser Pro Gly Arg Thr Arg Arg Ala Ile Ala
180 185 190

Ala Val Leu Ser Ala Ala Leu Leu Thr Gly Ile Pro Phe Tyr Trp Trp
195 200 205

Leu Asp Met Trp Arg Asp Thr Asp Ser Pro Arg Thr Leu Asp Glu Val
210 215 220

Leu Lys Trp Ala His Cys Leu Thr Val Tyr Phe Ile Pro Cys Gly Val
225 230 235 240

Phe Leu Val Thr Asn Ser Ala Ile Ile His Arg Leu Arg Arg Arg Gly
245 250 255

Arg Ser Gly Leu Gln Pro Arg Val Gly Lys Ser Thr Ala Ile Leu Leu
260 265 270

Gly Ile Thr Thr Leu Phe Thr Leu Leu Trp Ala Pro Arg Val Phe Val
275 280 285

Met Leu Tyr His Met Tyr Val Ala Pro Val His Arg Asp Trp Arg Val
290 295 300

His Leu Ala Leu Asp Val Ala Asn Met Val Ala Met Leu His Thr Ala
305 310 315 320

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Ala Asn Phe Gly Leu Tyr Cys Phe Val Ser Lys Thr Phe Arg Ala Thr
325 330 335

Val Arg Gln Val Ile His Asp Ala Tyr Leu Pro Cys Thr Leu Ala Ser
340 345 350

Gln Pro Glu Gly Met Ala Ala Lys Pro Val Met Glu Pro Pro Gly Leu
355 360 365

Pro Thr Gly Ala Glu Val
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Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
 35 40 45

Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
 50 55 60

Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
 65 70 75 80

Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
 85 90 95

Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
 100 105 110

Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
 115 120 125

Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
 130 135 140

Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
 145 150 155 160

Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
 165 170 175

Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
 180 185 190

Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
 195 200 205

Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
 210 215 220

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Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
225 230 235 240

Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
245 250 255

Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
260 265 270

Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
275 280 285

Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
290 295 300

Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305 310 315 320

Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
325 330 335

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340 345 350

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Asn Val Asn Gly Ser Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg
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Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe
 35 40 45

Gly Asn Leu Leu Val Met Ile Ser Ile Leu His Phe Lys Gln Leu His
 50 55 60

Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala Cys Ala Asp Phe Leu
 65 70 75 80

Val Gly Val Thr Val Met Pro Phe Ser Met Val Arg Thr Val Glu Ser
 85 90 95

Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe His Thr Cys Cys Asp
 100 105 110

Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu Cys Phe Ile Ser Ile
 115 120 125

Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val Tyr Pro Thr Lys Phe
 130 135 140

AREN0308.ST25.txt

Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro
145 150 155 160

Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Tyr Asp Asp Gly
165 170 175

Leu Glu Glu Leu Ser Asp Ala Leu Asn Cys Ile Gly Gly Cys Gln Thr
180 185 190

Val Val Asn Gln Asn Trp Val Leu Thr Asp Phe Leu Ser Phe Phe Ile
195 200 205

Pro Thr Phe Ile Met Ile Ile Leu Tyr Gly Asn Ile Phe Leu Val Ala
210 215 220

Arg Arg Gln Ala Lys Lys Ile Glu Asn Thr Gly Ser Lys Thr Glu Ser
225 230 235 240

Ser Ser Glu Ser Tyr Lys Ala Arg Val Ala Arg Arg Glu Arg Lys Ala
245 250 255

Ala Lys Thr Leu Gly Val Thr Val Val Ala Phe Met Ile Ser Trp Leu
260 265 270

Pro Tyr Ser Ile Asp Ser Leu Ile Asp Ala Phe Met Gly Phe Ile Thr
275 280 285

Pro Ala Cys Ile Tyr Glu Ile Cys Cys Trp Cys Ala Tyr Tyr Asn Ser
290 295 300

Ala Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp Phe Arg Lys
305 310 315 320

Ala Ile Lys Val Ile Val Thr Gly Gln Val Leu Lys Asn Ser Ser Ala
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Thr Met Asn Leu Phe Ser Glu His Ile
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<220>
<223> Novel Sequence

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Met Met Pro Phe Cys His Asn Ile Ile Asn Ile Ser Cys Val Lys Asn
1 5 10 15

Asn Trp Ser Asn Asp Val Arg Ala Ser Leu Tyr Ser Leu Met Val Leu
20 25 30

Ile Ile Leu Thr Thr Leu Val Gly Asn Leu Ile Val Ile Val Ser Ile
35 40 45

Ser His Phe Lys Gln Leu His Thr Pro Thr Asn Trp Leu Ile His Ser
50 55 60

Met Ala Thr Val Asp Phe Leu Leu Gly Cys Leu Val Met Pro Tyr Ser
65 70 75 80

Met Val Arg Ser Ala Glu His Cys Trp Tyr Phe Gly Glu Val Phe Cys
85 90 95

AREN0308.ST25.txt

Lys Ile His Thr Ser Thr Asp Ile Met Leu Ser Ser Ala Ser Ile Phe
100 105 110

His Leu Ser Phe Ile Ser Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro
115 120 125

Leu Arg Tyr Lys Ala Lys Met Asn Ile Leu Val Ile Cys Val Met Ile
130 135 140

Phe Ile Ser Trp Ser Val Pro Ala Val Phe Ala Phe Gly Met Ile Phe
145 150 155 160

Leu Glu Leu Asn Phe Lys Gly Ala Glu Glu Ile Tyr Tyr Lys His Val
165 170 175

His Cys Arg Gly Gly Cys Ser Val Phe Phe Ser Lys Ile Ser Gly Val
180 185 190

Leu Thr Phe Met Thr Ser Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys
195 200 205

Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile
210 215 220

Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly
225 230 235 240

Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val
245 250 255

Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val
260 265 270

Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Val
275 280 285

Leu Ile Trp Phe Gly Tyr Leu Asn Ser Thr Phe Asn Pro Met Val Tyr
290 295 300

Ala Phe Phe Tyr Pro Trp Phe Arg Lys Ala Leu Lys Met Met Leu Phe
305 310 315 320

Gly Lys Ile Phe Gln Lys Asp Ser Ser Arg Cys Lys Leu Phe Leu Glu
325 330 335

Leu Ser Ser

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<211> 1029
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 13
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cagctgcaact ctccaaccaa ttttctcatt gcctctctgg cctgtgctga cttcttggtg 240
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gccaaatttt gtactcttca cagttgctgt gatgtggcat tttgttactc ttctgtcctc 360
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accaagtcca ccgtgtctgt gtcgggaatt tgcacagcg tgcctggat tctgcctctc 480
acgtacagcg gtgctgtgtt ctacacaggt gtcaatgatg atgggctgga ggaattagta 540
agtgtcttca actgcgtagg tggctgtcaa attattgtaa gtcaaggctg ggtgttgata 600
gattttctgt tattcttcat acctaccctt gttatgataa ttctttacag taagattttt 660
cttatagcta aacaacaagc tataaaaatt gaaactacta gtagcaaagt agaatcatcc 720
tcagagagtt ataaaatcag agtggccaag agagagagga aagcagctaa aaccctgggg 780
gtcacggtag tagcatttgt tatttcatgg ttaccgtata cagttgatat attaattgat 840
gcctttatgg gcttcctgac ccctgcctat atctatgaaa tttgctgttg gagtgcttat 900
tataactcag ccatgaatcc tttgatttat gctctatttt atccttggtt taggaaagcc 960
ataaaactta ttttaagtgg agatgtttta aaggctagtt catcaacat tagttttatt 1020
ttagaataa 1029

<210> 14
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 14

Met Thr Ser Asn Phe Ser Gln Pro Val Val Gln Leu Cys Tyr Glu Asp
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Val Asn Gly Ser Cys Ile Glu Thr Pro Tyr Ser Pro Gly Ser Arg Val
20 25 30

Ile Leu Tyr Thr Ala Phe Ser Phe Gly Ser Leu Leu Ala Val Phe Gly
35 40 45

Asn Leu Leu Val Met Thr Ser Val Leu His Phe Lys Gln Leu His Ser
 50 55 60
 Pro Thr Asn Phe Leu Ile Ala Ser Leu Ala Cys Ala Asp Phe Leu Val
 65 70 75 80
 Gly Val Thr Val Met Leu Phe Ser Met Val Arg Thr Val Glu Ser Cys
 85 90 95
 Trp Tyr Phe Gly Ala Lys Phe Cys Thr Leu His Ser Cys Cys Asp Val
 100 105 110
 Ala Phe Cys Tyr Ser Ser Val Leu His Leu Cys Phe Ile Cys Ile Asp
 115 120 125
 Arg Tyr Ile Val Val Thr Asp Pro Leu Val Tyr Ala Thr Lys Phe Thr
 130 135 140
 Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro Leu
 145 150 155 160
 Thr Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Asn Asp Asp Gly Leu
 165 170 175
 Glu Glu Leu Val Ser Ala Leu Asn Cys Val Gly Gly Cys Gln Ile Ile
 180 185 190
 Val Ser Gln Gly Trp Val Leu Ile Asp Phe Leu Leu Phe Phe Ile Pro
 195 200 205
 Thr Leu Val Met Ile Ile Leu Tyr Ser Lys Ile Phe Leu Ile Ala Lys
 210 215 220
 Gln Gln Ala Ile Lys Ile Glu Thr Thr Ser Ser Lys Val Glu Ser Ser
 225 230 235 240
 Ser Glu Ser Tyr Lys Ile Arg Val Ala Lys Arg Glu Arg Lys Ala Ala
 245 250 255
 Lys Thr Leu Gly Val Thr Val Leu Ala Phe Val Ile Ser Trp Leu Pro
 260 265 270
 Tyr Thr Val Asp Ile Leu Ile Asp Ala Phe Met Gly Phe Leu Thr Pro
 275 280 285
 Ala Tyr Ile Tyr Glu Ile Cys Cys Trp Ser Ala Tyr Tyr Asn Ser Ala
 290 295 300

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Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp Phe Arg Lys Ala
305 310 315 320

Ile Lys Leu Ile Leu Ser Gly Asp Val Leu Lys Ala Ser Ser Ser Thr
325 330 335

Ile Ser Leu Phe Leu Glu
340

<210> 15
<211> 1062
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 15
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ttaccagcaa atatcttgac agtgatcatc ctctccagc tggaggcaag aagacagaag 180
tcctcctaca actatctctt ggcactcgtc gctgccgaca tcttggtcct ctttttcata 240
gtgtttgtgg acttcctggt ggaagatttc atcttgaaca tgcagatgcc tcagggtccc 300
gacaagatca tagaagtgtc ggaattctca tccatccaca cctccatatt gattactgta 360
ccgttaacca ttgacaggta tctcgtgtc tgccaccgc tcaagtacca cacggtctca 420
taccagccc gcacccggaa agtcattgta agtggtttaca tcacctgctt cctgaccagc 480
atcccctatt actggtggcc caacatctgg actgaagact acatcagcac ctctgtgcat 540
cacgtcctca tctggatcca ctgcttcacc gtctacctgg tgccctgctc catcttcttc 600
atcttgaact caatcattgt gtacaagctc aggaggaaga gcaattttcg tctccgtggc 660
tactccacgg ggaagaccac cgccatcttg ttcaccatta cctccatctt tgccacactt 720
tgggccccc gcacatcat gattctttac cacctctatg gggcgcccat ccagaaccgc 780
tggtggtgac acatcatgtc cgacattgcc aacatgctag ccttctgaa cacagccatc 840
aacttcttcc tctactgctt catcagcaag cgttccgca ccatggcagc cgccacgctc 900
aaggtttct tcaagtcca gaagcaacct gtacagttct acaccaatca taacttttcc 960
ataacaagta gccctggat ctgcgggca aactcacact gcatcaagat gctggtgtac 1020
cagtatgaca aaaatggaaa acctataaaa gtatccccgt ga 1062

<210> 16
<211> 353
<212> PRT
<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 16

Met Glu His Thr His Ala His Leu Ala Ala Asn Ser Ser Leu Ser Trp
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Trp Ser Pro Gly Ser Ala Cys Gly Leu Gly Phe Val Pro Val Val Tyr
 20 25 30

Tyr Ser Leu Leu Leu Cys Leu Gly Leu Pro Ala Asn Ile Leu Thr Val
 35 40 45

Ile Ile Leu Ser Gln Leu Val Ala Arg Arg Gln Lys Ser Ser Tyr Asn
 50 55 60

Tyr Leu Leu Ala Leu Ala Ala Ala Asp Ile Leu Val Leu Phe Phe Ile
 65 70 75 80

Val Phe Val Asp Phe Leu Leu Glu Asp Phe Ile Leu Asn Met Gln Met
 85 90 95

Pro Gln Val Pro Asp Lys Ile Ile Glu Val Leu Glu Phe Ser Ser Ile
 100 105 110

His Thr Ser Ile Trp Ile Thr Val Pro Leu Thr Ile Asp Arg Tyr Ile
 115 120 125

Ala Val Cys His Pro Leu Lys Tyr His Thr Val Ser Tyr Pro Ala Arg
 130 135 140

Thr Arg Lys Val Ile Val Ser Val Tyr Ile Thr Cys Phe Leu Thr Ser
 145 150 155 160

Ile Pro Tyr Tyr Trp Trp Pro Asn Ile Trp Thr Glu Asp Tyr Ile Ser
 165 170 175

Thr Ser Val His His Val Leu Ile Trp Ile His Cys Phe Thr Val Tyr
 180 185 190

Leu Val Pro Cys Ser Ile Phe Phe Ile Leu Asn Ser Ile Ile Val Tyr
 195 200 205

Lys Leu Arg Arg Lys Ser Asn Phe Arg Leu Arg Gly Tyr Ser Thr Gly
 210 215 220

Lys Thr Thr Ala Ile Leu Phe Thr Ile Thr Ser Ile Phe Ala Thr Leu
 225 230 235 240

Trp Ala Pro Arg Ile Ile Met Ile Leu Tyr His Leu Tyr Gly Ala Pro

245

250

255

Ile Gln Asn Arg Trp Leu Val His Ile Met Ser Asp Ile Ala Asn Met
 260 265 270

Leu Ala Leu Leu Asn Thr Ala Ile Asn Phe Phe Leu Tyr Cys Phe Ile
 275 280 285

Ser Lys Arg Phe Arg Thr Met Ala Ala Ala Thr Leu Lys Ala Phe Phe
 290 295 300

Lys Cys Gln Lys Gln Pro Val Gln Phe Tyr Thr Asn His Asn Phe Ser
 305 310 315 320

Ile Thr Ser Ser Pro Trp Ile Ser Pro Ala Asn Ser His Cys Ile Lys
 325 330 335

Met Leu Val Tyr Gln Tyr Asp Lys Asn Gly Lys Pro Ile Lys Val Ser
 340 345 350

Pro

<210> 17
 <211> 969
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

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 ggactgacag gaaacgcggg agtgctctgg ctctggggct accgcatgcg caggaacgct 180
 gtctccatct acatcctcaa cctggccgca gcagacttcc tcttctcag cttccagatt 240
 atacgttcgc cattacgcct catcaatatc agccatctca tccgcaaaat cctcgtttct 300
 gtgatgacct ttccctactt tacaggcctg agtatgctga gcgccatcag caccgagcgc 360
 tgectgtctg ttctgtggcc catctggtac cgctgccgcc gccccacaca cctgtcagcg 420
 gtcgtgtgtg tctgtctctg gggcctgtcc ctgctgttta gtatgctgga gtggagggtc 480
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 gtgcgctggc tgattttttt atgtgtgggt ctctgtgttt ccagcctggg cctgctgggc 600
 aggatcctct gtggatcccg gaagatgccg ctgaccaggc tgtacgtgac catcctgctc 660
 acagtgtctg tcttctcctc ctgcgcctg cccttcggca ttctgggggc cctaatttac 720
 aggatgcacc tgaatttga agtcttatat tgctatgttt atctggtttg catgtccctg 780

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tcctctctaa acagtagtgc caaccccatc atttacttct tcgtgggctc ctttaggcag 840
cgtcaaaata ggcagaacct gaagctgggt ctccagaggg ctctgcagga caagcctgag 900
gtggataaag gtgaagggca gcttcctgag gaaagcctgg agctgtcggg aagcagattg 960
gggccatga 969

<210> 18
<211> 322
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 18

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Gly Arg Glu Glu Thr Pro Cys Tyr Asn Gln Thr Leu Ser Phe Thr Val
20 25 30

Leu Thr Cys Ile Ile Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val
35 40 45

Leu Trp Leu Leu Gly Tyr Arg Met Arg Arg Asn Ala Val Ser Ile Tyr
50 55 60

Ile Leu Asn Leu Ala Ala Asp Phe Leu Phe Leu Ser Phe Gln Ile
65 70 75 80

Ile Arg Ser Pro Leu Arg Leu Ile Asn Ile Ser His Leu Ile Arg Lys
85 90 95

Ile Leu Val Ser Val Met Thr Phe Pro Tyr Phe Thr Gly Leu Ser Met
100 105 110

Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile
115 120 125

Trp Tyr Arg Cys Arg Arg Pro Thr His Leu Ser Ala Val Val Cys Val
130 135 140

Leu Leu Trp Gly Leu Ser Leu Leu Phe Ser Met Leu Glu Trp Arg Phe
145 150 155 160

Cys Asp Phe Leu Phe Ser Gly Ala Asp Ser Ser Trp Cys Glu Thr Ser
165 170 175

Asp Phe Ile Pro Val Ala Trp Leu Ile Phe Leu Cys Val Val Leu Cys

180

185

190

Val Ser Ser Leu Val Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Lys
195 200 205

Met Pro Leu Thr Arg Leu Tyr Val Thr Ile Leu Leu Thr Val Leu Val
210 215 220

Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile Leu Gly Ala Leu Ile Tyr
225 230 235 240

Arg Met His Leu Asn Leu Glu Val Leu Tyr Cys His Val Tyr Leu Val
245 250 255

Cys Met Ser Leu Ser Ser Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr
260 265 270

Phe Phe Val Gly Ser Phe Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys
275 280 285

Leu Val Leu Gln Arg Ala Leu Gln Asp Lys Pro Glu Val Asp Lys Gly
290 295 300

Glu Gly Gln Leu Pro Glu Glu Ser Leu Glu Leu Ser Gly Ser Arg Leu
305 310 315 320

Gly Pro

<210> 19
<211> 969
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 19
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gcgctgacag gaaacgcggt tgtgctctgg ctctctgggt gccgcatgcg caggaacgct 180
gtctccatct acatcctcaa cctggtcgcg gccgacttcc tcttccttag cggccacatt 240
atatgttcgc cgttacgcct catcaatcgc cgccatccca tctccaaaat cctcagtcct 300
gtgatgacct ttccctactt tataggccta agcatgctga gcgccatcag caccgagcgc 360
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gtcatgtgtg tcctgtctctg ggccctgtcc ctgctgcgga gtatcctgga gtggatgttc 480
tgtgacttcc tgttttagtg tgctgattct gtttggtgtg aaacgtcaga tticattaca 540

AREN0308.ST25.txt

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acagtgtctg tcttcctcct ctgtggcctg ccctttggca ttcagtgggc cctgttttcc 720
aggatccacc tggattggaa agtcttattt tgcatgtgc atctagtttc cattttcctg 780
tccgctctta acagcagtgc caaccccatc atttacttct tcgtgggctc ctttaggcag 840
cgtcaaaata ggcagaacct gaagctggtt ctccagaggg ctctgcagga cagcctgag 900
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gagcagtga 969

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<210> 20
 <211> 322
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 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 20

Met Asp Ser Thr Ile Pro Val Leu Gly Thr Glu Leu Thr Pro Ile Asn
 1 5 10 15

Gly Arg Glu Glu Thr Pro Cys Tyr Lys Gln Thr Leu Ser Phe Thr Gly
 20 25 30

Leu Thr Cys Ile Val Ser Leu Val Ala Leu Thr Gly Asn Ala Val Val
 35 40 45

Leu Trp Leu Leu Gly Cys Arg Met Arg Arg Asn Ala Val Ser Ile Tyr
 50 55 60

Ile Leu Asn Leu Val Ala Ala Asp Phe Leu Phe Leu Ser Gly His Ile
 65 70 75 80

Ile Cys Ser Pro Leu Arg Leu Ile Asn Ile Arg His Pro Ile Ser Lys
 85 90 95

Ile Leu Ser Pro Val Met Thr Phe Pro Tyr Phe Ile Gly Leu Ser Met
 100 105 110

Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Ile Leu Trp Pro Ile
 115 120 125

Trp Tyr His Cys Arg Arg Pro Arg Tyr Leu Ser Ser Val Met Cys Val
 130 135 140

Leu Leu Trp Ala Leu Ser Leu Leu Arg Ser Ile Leu Glu Trp Met Phe

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145 150 155 160

Cys Asp Phe Leu Phe Ser Gly Ala Asp Ser Val Trp Cys Glu Thr Ser
165 170 175

Asp Phe Ile Thr Ile Ala Trp Leu Val Phe Leu Cys Val Val Leu Cys
180 185 190

Gly Ser Ser Leu Val Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Lys
195 200 205

Met Pro Leu Thr Arg Leu Tyr Val Thr Ile Leu Leu Thr Val Leu Val
210 215 220

Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Ala Leu Phe Ser
225 230 235 240

Arg Ile His Leu Asp Trp Lys Val Leu Phe Cys His Val His Leu Val
245 250 255

Ser Ile Phe Leu Ser Ala Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr
260 265 270

Phe Phe Val Gly Ser Phe Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys
275 280 285

Leu Val Leu Gln Arg Ala Leu Gln Asp Thr Pro Glu Val Asp Glu Gly
290 295 300

Gly Gly Trp Leu Pro Gln Glu Thr Leu Glu Leu Ser Gly Ser Arg Leu
305 310 315 320

Glu Gln

<210> 21
<211> 26
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<400> 21
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26

<210> 22
<211> 25
<212> DNA
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<220>

<223> Novel Sequence

<400> 22

ctgcgtccac cagagtcacg tctcc

25

<210> 23

<211> 26

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<400> 23

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26

<210> 24

<211> 31

<212> DNA

<213> Artificial Sequence

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<400> 24

gtttgtggct aacggcaca aacacaattc c

31

<210> 25

<211> 28

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<400> 25

ggtaccacaa tgacaatcac cagcgtcc

28

<210> 26

<211> 29

<212> DNA

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<220>

<223> Novel Sequence

<400> 26

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29

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<212> DNA

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<400> 27

gcagtgtagc ggtcaaccgt gagcagg

27

<210> 28
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<400> 29
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<210> 30
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<210> 31
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<220>
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<400> 31
 ggaatgtcca ctgaatgcgc gcgg 24

<210> 32
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<400> 32
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<210> 33
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<210> 34
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<400> 34
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<210> 35
<211> 29
<212> DNA
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<220>
<223> Novel Sequence

<400> 35
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<210> 36
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 36
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<210> 37
<211> 29
<212> DNA
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<400> 37
aaacaacaaa cagcagaacc atgaccagc          29

<210> 38
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<400> 38

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<220>
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<400> 39
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26

<210> 40
<211> 29
<212> DNA
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<220>
<223> Novel Sequence

<400> 40
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29

<210> 41
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 41
gcgctcatgg agcacacgca cgccac

27

<210> 42
<211> 25
<212> DNA
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<220>
<223> Novel Sequence

<400> 42
gaggcagtag ttgccacacc tatgg

25

<210> 43
<211> 29
<212> DNA
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<220>
<223> Novel Sequence

<400> 43
catctggttt gtgttcccag gggcaccag

29

<210> 44
<211> 32

<212> DNA
<213> Artificial Sequence

<220>
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<400> 44
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32

<210> 45
<211> 25
<212> DNA
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<220>
<223> Novel Sequence

<400> 45
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<210> 46
<211> 27
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<400> 46
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<210> 47
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<213> Artificial Sequence

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<400> 47

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1 5

<210> 48
<211> 5
<212> PRT
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<220>
<223> Novel Sequence

<400> 48

Glu Tyr Asn Leu Val
1 5

<210> 49
<211> 5
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<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 49

Asp Cys Gly Leu Phe
1 5

<210> 50

<211> 34

<212> DNA

<213> Artificial Sequence

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<400> 50

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53

<210> 52

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 52

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25

<210> 53

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 53

ctgcgtccac cagagtcacg tctcc

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<210> 54

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Novel Sequence

<400> 54

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26

<210> 55

<211> 31

<212> DNA

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<223> Novel Sequence

<400> 55

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31

<210> 56

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 56

ctgctcacgg ttgaccgcta cactgc

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<210> 57

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 57

gtggccatga gccaccctga gctcc

25

<210> 58

<211> 20

<212> DNA

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<223> Novel Sequence

<400> 58

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<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 59

cttcttctcc gacgtcaagg

20

<210> 60
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 60
 cttcttctcc gacgtcaagg 20

<210> 61
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